

RAW SEQUENCE LISTING

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Application Serial Number: 10/525, 326 A
Source: LEW0
Date Processed by STIC: 07/10/2006

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DATE: 07/10/2006

PATENT APPLICATION: US/10/525,326A

TIME: 12:31:54

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Output Set: N:\CRF4\07072006\J525326A.raw

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3 <110> APPLICANT: SAKI, Mayumi
4     NONAKA, Hiromi
5     MIYAJI, Hiromasa
6     HIURA, Naoko
7     MANABE, Haruhiko
8     MATSUMURA, Tsutomu
9     ARAI, Hitoshi
10    SASAKI, Katsutoshi
11    KOBATAKE, Choei
12    KUBOYAMA, Takeshi
13
15 <120> TITLE OF INVENTION: AGENT FOR PREVENTION AND/OR TREATMENT OF ASTHMA
17 <130> FILE REFERENCE: 506.44792X00
19 <140> CURRENT APPLICATION NUMBER: 10/525,326A
20 <141> CURRENT FILING DATE: 2005-02-22
22 <150> PRIOR APPLICATION NUMBER: JP 2002/241523
23 <151> PRIOR FILING DATE: 2002-08-22
25 <160> NUMBER OF SEQ ID NOS: 18
27 <170> SOFTWARE: PatentIn Ver. 2.1
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31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
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44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
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56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
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78 <212> TYPE: DNA
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81 <220> FEATURE:
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84 <400> SEQUENCE: 5
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88 <210> SEQ ID NO: 6
89 <211> LENGTH: 40
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
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159           20           25           30
161 Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln
162           35           40           45
164 Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu
165   50           55           60
167 Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His
168   65           70           75           80
170 Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile
171           85           90           95
173 Phe Tyr Thr Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser
174           100          105          110
176 Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu
177           115          120          125
179 Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr
180           130          135          140
182 Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg
183 145           150          155          160
185 Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly
186           165          170          175
188 Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe
189           180          185          190
191 Pro Trp Ala Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val
192           195          200          205
194 Arg Gly Ser Val Ser Thr Glu Arg Gln Glu Lys Ala Lys Ile Lys Arg
195           210          215          220
197 Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr
198 225           230          235          240
200 His Val Leu Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp
201           245          250          255
203 Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu
204           260          265          270
206 Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu
207           275          280          285
209 Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu

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210      290      295      300
212 Leu Arg Phe Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser
213 305      310      315      320
215 Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys
216      325      330      335
218 Ala Met Thr Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln
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221 Val Gln Leu Lys Met Leu Pro Pro Ala Gln
222      355      360
225 <210> SEQ ID NO: 12
226 <211> LENGTH: 2932
227 <212> TYPE: DNA
228 <213> ORGANISM: Homo sapiens
230 <400> SEQUENCE: 12
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233 agaccttact cacctccttc ctgtttccta agactccttc ctgccgtcca cagaccgagc 180
234 cttttatctt tgtccaccct gtgccagaca cctccttttc cagaaccttc tccttactgg 240
235 tgaccttact tatctctgtt gctttctggg gtcctagga atgccagcac tcccacccac 300
236 attgcctgaa ctttccaaca ctccctagct gcgctgtgtc ctatctcaac acttcctcat 360
237 gtatttcttg tgtcttctag aacattcccc cgccattatt acttcaatat ggctacacat 420
238 acttcctaatt tgccctgcaa accatctcct tctcaccatt gcccagcgat gctttcgtct 480
239 cctccataaaa cactcccggg gaccaatttt tgtgtcacc ccatactccc tcgttgacac 540
240 actgactcca tacataacct ccttgaaaaa cctctttatt aatctcacca tctccagac 600
241 ttcctcctctg tcataattcc atccctcctc caacttttcc ctctcaagct ctgcccttcc 660
242 cagcccagcc cagcctaccc aacctcatct ctccctgta gaccacatcc caccatgttc 720
243 ccctgagcct ccaaggaagg ggctcagggg gcccctggc ctcccgtccc ctgtggcccc 780
244 acagcccccg tgggcccagg gaagcgcccc agaagccgaa gtgccacc atg ggc aac 838
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246      Met Gly Asn
247      1
248 cac acg tgg gag ggc tgc cac gtg gac tcg cgc gtg gac cac ctc ttt 886
249 His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp His Leu Phe
250 5      10      15
252 ccg cca tcc ctc tac atc ttt gtc atc ggc gtg ggg ctg ccc acc aac 934
253 Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu Pro Thr Asn
254 20      25      30      35
256 tgc ctg gct ctg tgg gcg gcc tac cgc cag gtg caa cag cgc aac gag 982
257 Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln Arg Asn Glu
258 40      45      50
260 ctg ggc gtc tac ctg atg aac ctc agc atc gcc gac ctg ctg tac atc 1030
261 Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu Leu Tyr Ile
262 55      60      65
264 tgc acg ctg ccg ctg tgg gtg gac tac ttc ctg cac cac gac aac tgg 1078
265 Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His Asp Asn Trp
266 70      75      80
268 atc cac ggc ccc ggg tcc tgc aag ctc ttt ggg ttc atc ttc tac acc 1126
269 Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile Phe Tyr Thr
270 85      90      95
272 aat atc tac atc agc atc gcc ttc ctg tgc tgc atc tcg gtg gac cgc 1174

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273 Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser Val Asp Arg
274 100 105 110 115
276 tac ctg gct gtg gcc cac cca ctc cgc ttc gcc cgc ctg cgc cgc gtc 1222
277 Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu Arg Arg Val
278 120 125 130
280 aag acc gcc gtg gcc gtg agc tcc gtg gtc tgg gcc acg gag ctg ggc 1270
281 Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr Glu Leu Gly
282 135 140 145
284 gcc aac tcg gcg ccc ctg ttc cat gac gag ctc ttc cga gac cgc tac 1318
285 Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg Asp Arg Tyr
286 150 155 160
288 aac cac acc ttc tgc ttt gag aag ttc ccc atg gaa ggc tgg gtg gcc 1366
289 Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly Trp Val Ala
290 165 170 175
292 tgg atg aac ctc tat cgg gtg ttc gtg ggc ttc ctc ttc ccg tgg gcg 1414
293 Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe Pro Trp Ala
294 180 185 190 195
296 ctc atg ctg ctg tcg tac cgg ggc atc ctg cgg gcc gtg cgg ggc agc 1462
297 Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val Arg Gly Ser
298 200 205 210
300 gtg tcc acc gag cgc cag gag aag gcc aag atc aag cgg ctg gcc ctc 1510
301 Val Ser Thr Glu Arg Gln Glu Lys Ala Lys Ile Lys Arg Leu Ala Leu
302 215 220 225
304 agc ctc atc gcc atc gtg ctg gtc tgc ttt gcg ccc tat cac gtg ctc 1558
305 Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr His Val Leu
306 230 235 240
308 ttg ctg tcc cgc agc gcc atc tac ctg ggc cgc ccc tgg gac tgc ggc 1606
309 Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp Asp Cys Gly
310 245 250 255
312 ttc gag gag cgc gtc ttt tct gca tac cac agc tca ctg gct ttc acc 1654
313 Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu Ala Phe Thr
314 260 265 270 275
316 agc ctc aac tgt gtg gcg gac ccc atc ctc tac tgc ctg gtc aac gag 1702
317 Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu Val Asn Glu
318 280 285 290
320 ggc gcc cgc agc gat gtg gcc aag gcc ctg cac aac ctg ctc cgc ttt 1750
321 Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu Leu Arg Phe
322 295 300 305
324 ctg gcc agc gac aag ccc cag gag atg gcc aat gcc tcg ctc acc ctg 1798
325 Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser Leu Thr Leu
326 310 315 320
328 gag acc cca ctc acc tcc aag agg aac agc aca gcc aaa gcc atg act 1846
329 Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys Ala Met Thr
330 325 330 335
332 ggc agc tgg gcg gcc act ccg ccc tcc cag ggg gac cag gtg cag ctg 1894
333 Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln Val Gln Leu
334 340 345 350 355
336 aag atg ctg ccg cca gca caa tga accccgagtg gcacagaatc cccagttttc 1948
337 Lys Met Leu Pro Pro Ala Gln

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VERIFICATION SUMMARY

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